

Please cite:

```
/tmp/fastCAygaWej: 995 aa
```

>SEQ ID NO:2

```
vs /tmp/fastaDAazgaWej library
```

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searching /tmp/fastaDAAzgaWej library
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1008 residues in 1 sequences

FASTA (3.34 January 2000) function [optimized, BL50 matrix (15:-5)] ktup: 2

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join: 39, opt: 27, gap-pen: -12/ -2, width: 16
```

Scan time: 0.034

The best scores are:

The best scores are:

					opt
M13699	ACCESSION:	M13699	NID:	gi 180255 gb M13699.	(1008) 2671

>>M13699 ACCESSION:M13699 NID: gi 180255 gb M13699.1 HUM (1008 aa)

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initn: 1414 init1: 972 opt: 2671
```

Smith-Waterman score: 3980; 57.002% identity in 1014 aa overlap (1-992:1-1008)

```

              10      20      30      40      50
SEQ      MKILILGIFLFLCSSPGWAIDRHCYIGIEESIWNYPSPGKNMLNEKPFSEDL-----FLQ
          ::::::::::::::: .: :::: :. :::: .. .: .: : : .:
M13699   MKILILGIFLFLCSTPAWAKEKHYYIGIIETTWDYA---SDHGEKKLISVDTEHSNIYQL
              10      20      30      40      50

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      60      70      80      90     100     110
SEQ  GGQARKSFVFKKALYFYQYTDNTFQRIIEKPSWLGFLGPMIKAETGDFIYVHVKNNASRAY
      . : . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . .
M13699 NGPDRIGRLYKKALYLQYTDETFRTTIEKPVWLGFLGPIIKAETGDKVYVHLKNLASRPY
      60      70      80      90     100     110

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	120	130	140	150	160	170
SEQ	SYHPHGLTYSKENEAHGAIYPDNTTGLQKEVEYLEPGKQYTYKWYVEEHQGPSPDNCV					

M13699	TFHSHGITYYKEHE--GAIYPDNTTDFQRADDKVYPGEQYTYMLLATEEQSPGEGDGNVCV					
	120	130	140	150	160	170

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      180      190      200      210      220      230
SEQ    TRIYHSHIDTARDVASGLIGPILTKRGTNGDTEKDIDRSSFLMFSTTDESRSWYSDEN
      :::::::::: .::::::::: :: . . . :: :: .::::::::: :: . .
M13699 TRIYHSHIDAPKDIASGLIGPLIICKKDSLDKEKEKHIDREFVVMFSVVDENFSWYLEDN
      180      190      200      210      220      230

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	240	250	260	270	280	290
SEQ	IRAF-TESGKINTSDPRFEESMSMQSINGYIYGNLPNLTMCAEDRVQWYFVGMGGVADIH					
	...	:	...	:	:	:
M13699	IKTYCSEPEKVDKDNEFDQESNRMYSVNGYTFGSLPGLSMCAEDRVKWYLFMGNEVDVH					
	240	250	260	270	280	290

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      300      310      320      330      340      350
SEQ      PVYLRGQTLISRNHRKDTIMLFPSSEDAFMVAKAPGVWMLGCQ----IHESMQAFFKVS
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : . . . . .
M13699  AAFFHGQALTNKNYRIDTINLFPATLFDAYMVAQNPGEWMLSCQNLNHLKAGLQAFFQVQ
      300      310      320      330      340      350

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	360	370	380	390	400	410
SEQ	NCQKPST	EAFVTG	THVIHY	YIAAKE	ILWNYA	PSGIDFF

M13699	ECNKSS	KDNIRG	KHVRHY	YIAAEE	IWNYA	PSGIDIFT
	360	370	380	390	400	410

	420	430	440	450	460
SEQ	IGGTYK	KLIYRE	YTDASF	QTQKAR	---EEH

M13699	IGGSYK	KLIVRE	YTDASF	TNRKER	GPREEH
	420	430	440	450	460

	470	480	490	500	510	520
SEQ	QPPGLH	YNKSN	EGLFYE	---TPG	G-STPP	SSHVSP

M13699	EPIGV	RFNKN	NEGTY	YSPNYP	QSRSP	PPSASH
	480	490	500	510	520	530

	530	540	550	560	570	580
SEQ	TWFFY	SSVNG	KKDINS	GLLGPL	LCRNGS	LGDDGK

M13699	AKMY	SAVD	PTKDIF	TGLIGP	MKICKK	GSLHAN
	540	550	560	570	580	590

	590	600	610	620	630	640
SEQ	N-RTFI	TEPEN	IDKED	TDCQAS	NKMY	SINGYM

M13699	NIRMF	TAPDQ	VDKEDE	FQESNK	MHSMN	GFMYGN
	600	610	620	630	640	650

	650	660	670	680	690	700
SEQ	HGIYF	SGNTFT	SLGARR	DTIPMF	PYTSQT	LLMTPD

M13699	HGIYF	SGNTYL	WRGER	RDANLF	PQTSLT	LHMWPD
	660	670	680	690	700	710

	710	720	730	740	750	760
SEQ	RQCGK	PNPDQ	TQYQEE	KIIITIA	AEME	WDYS

M13699	NQCR	RQSE	DSTFY	LGERTY	-IAA	VEW
	720	730	740	750	760	770

	770	780	790	800	810	820
SEQ	LGSKY	KKVLY	RQYDD	NFTNQT	KRNEGE	KHLDIL

M13699	IGSKY	KKVVY	RQYTD	STFRVP	VERKAE	EEHLG
	780	790	800	810	820	830

	830	840	850	860	870	880
SEQ	HAHGV	KTNNS	TVVPTQ	PGEIQI	YTWQIP	DRGTSL

M13699	HAHGV	QTES	STVTP	TLPGET	LYVWKI	PERSGA
	840	850	860	870	880	890

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      890      900      910      920      930
SEQ    GPLSVCR----KDINPN-IVHRVLHFMIFDENESWYFEDSINTYASKPNKVDKENDNFQL
      ::: ::: : ::: .. : : : : : : : : : : : : : : : : : : : : : : : :
M13699 GPLIVCRRPYLKVFNPRRKLEFALLFLVFDENESWYLDNKTYS DHPEKVNKDDEEFIE
      900      910      920      930      940      950

      940      950      960      970      980      990
SEQ    SNQMHAINGRLFGNNQGITFHVGDVVNWYLLIGIGNEADLHTVHFHGHHSFEYKHKYLI
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M13699 SNKMHAINGRMFGNLQGLTMHVGDEVNWYLMGMGNEIDLHTVHFHGHHSFQYKHR
      960      970      980      990      1000

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995 residues in 1 query sequences

1008 residues in 1 library sequences

Scomplib [version 3.3t05 March 30, 2000]

start: Wed Sep 18 11:18:07 2002 done: Wed Sep 18 11:18:08 2002

Scan time: 0.034 Display time: 1.433

Function used was FASTA